

Sequence Range: 1 to 494

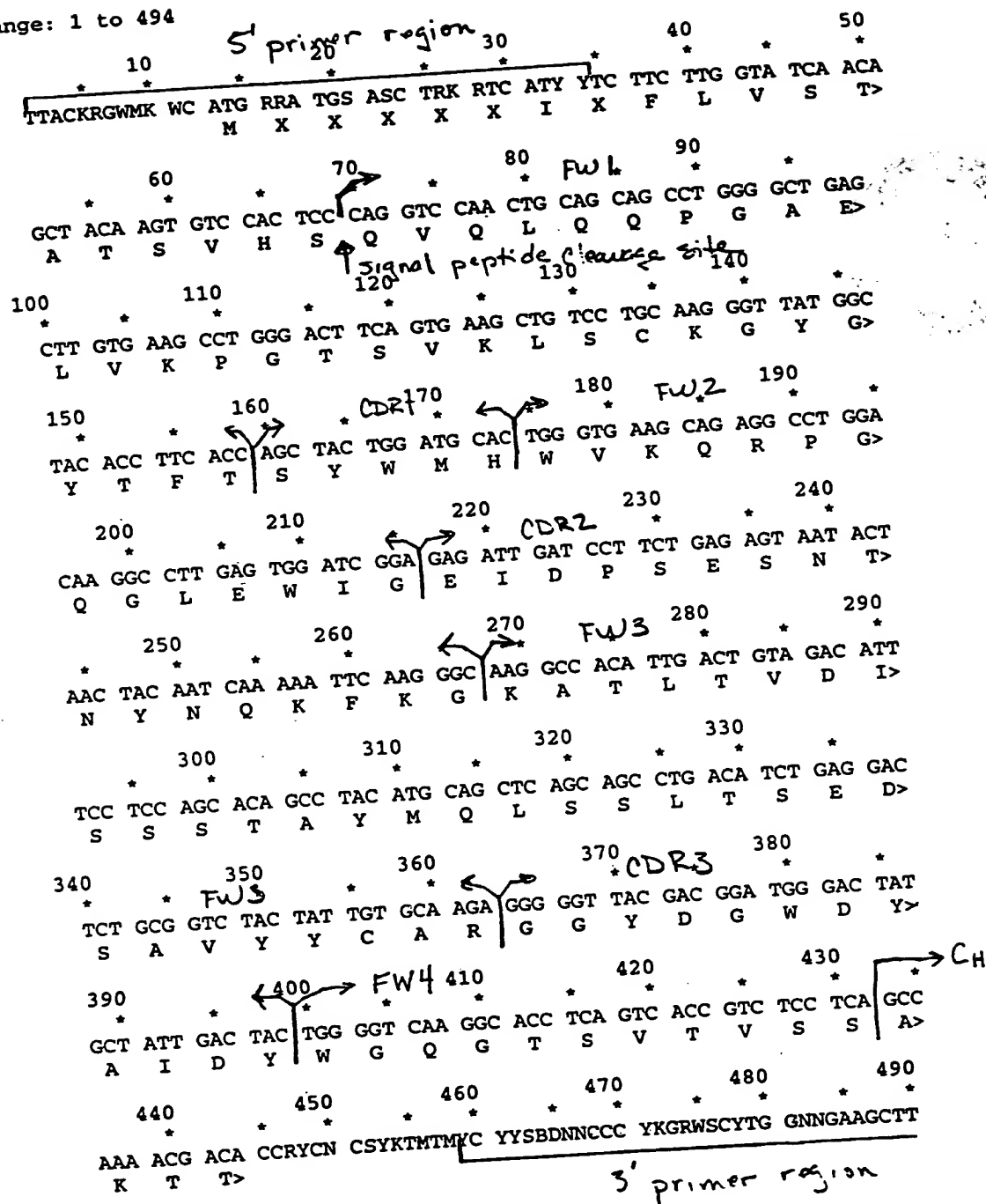


FIGURE 1

Sequence Range: 1 to 428

```

      10      20      30      40      50
      *      *      *      *      *
      *      *      *      *      *
TTACTTGACG ACTCGGG ATG GGA TGG AGC TAT ATC ATC TTC TTC TTG GTA TCA
      M      G      W      S      Y      I      I      F      F      L      V      S>

      60      70      80      90      100
      *      *      *      *      *
      *      *      *      *      *
ACA GCT ACA AGT GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG GCT
      T      A      T      S      V      H      S      Q      V      Q      L      Q      Q      P      G      A>

      110      120      130      140
      *      *      *      *      *
      *      *      *      *      *
GAG CTT GTG AAG CCT GGG ACT TCA GTG AAG CTG TCC TGC AAG GGT TAT
      E      L      V      K      P      G      T      S      V      K      L      S      C      K      G      Y>

      150      160      170      180      190
      *      *      *      *      *
      *      *      *      *      *
GGC TAC ACC TTC ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT
      G      Y      T      F      T      S      Y      W      M      H      W      V      K      Q      R      P>

      200      210      220      230      240
      *      *      *      *      *
      *      *      *      *      *
GGA CAA GGC CTT GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT
      G      Q      G      L      E      W      I      G      E      I      D      P      S      E      S      N>

      250      260      270      280      290
      *      *      *      *      *
      *      *      *      *      *
ACT AAC TAC AAT CAA AAA TTC AAG GGC AAG GCC ACA TTG ACT GTA GAC
      T      N      Y      N      Q      K      F      K      G      K      A      T      L      T      V      D>

      300      310      320      330      340
      *      *      *      *      *
      *      *      *      *      *
ATT TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG
      I      S      S      S      T      A      Y      M      Q      L      S      S      L      T      S      E>

      350      360      370      380
      *      *      *      *      *
      *      *      *      *      *
GAC TCT GCG GTC TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC
      D      S      A      V      Y      Y      C      A      R      G      G      Y      D      G      W      D>

      390      400      410      420
      *      *      *      *      *
      *      *      *      *      *
TAT GCT ATT GAC TAC TGG GGT CAA GGC ACA TCA GTC ACC
      Y      A      I      D      Y      W      G      Q      G      T      S      V      T>

```

FIGURE 2

Sequence Range: 1 to 535

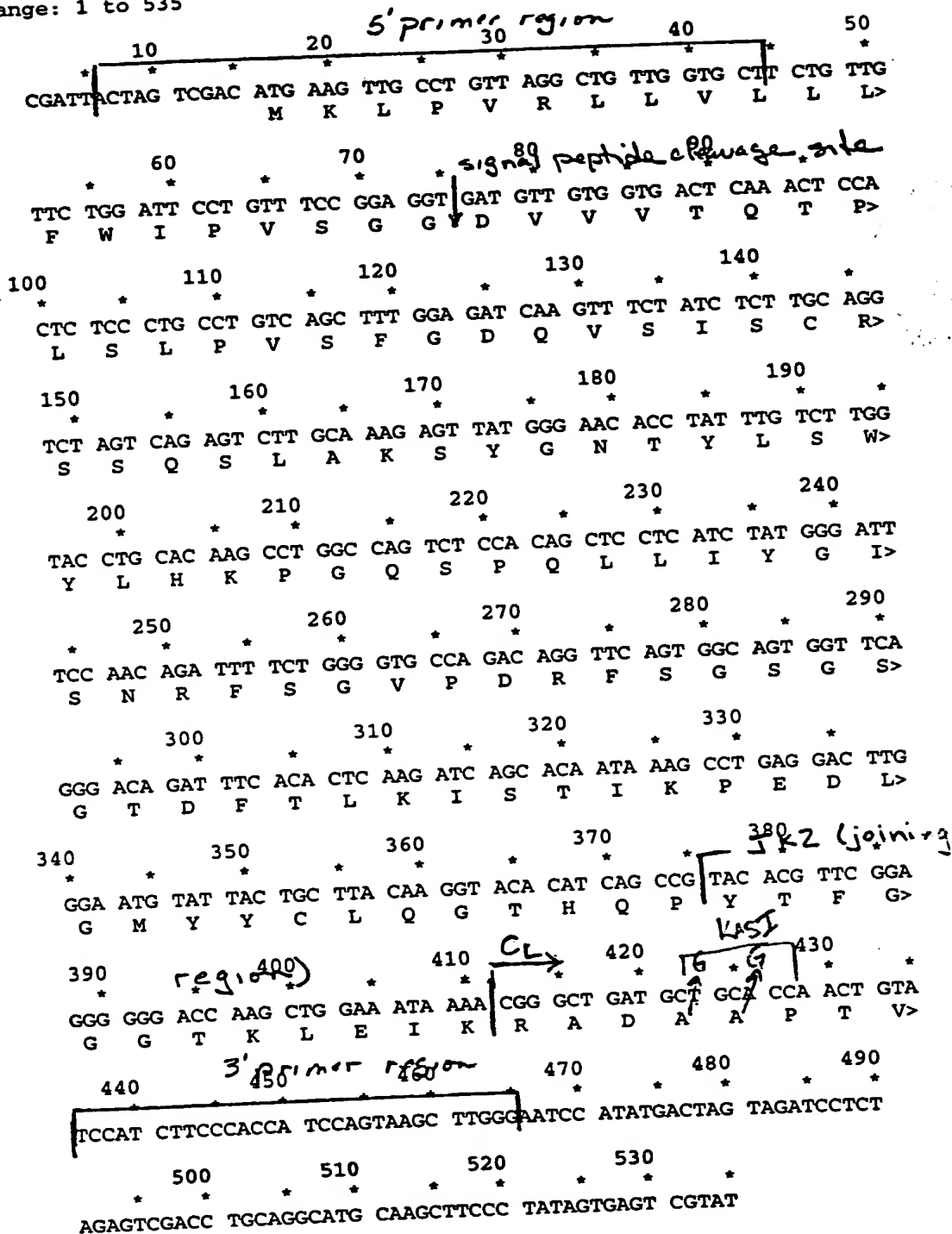


FIGURE 3

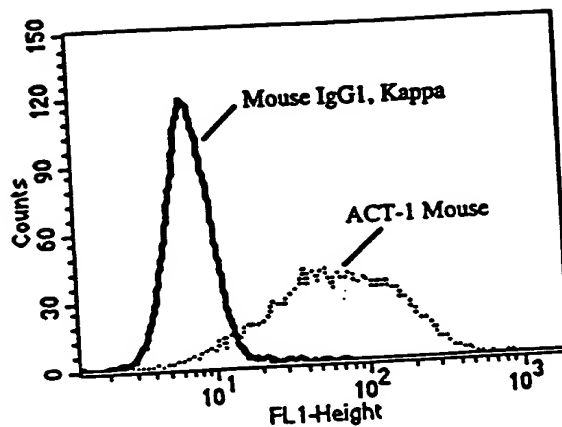


FIGURE 4A

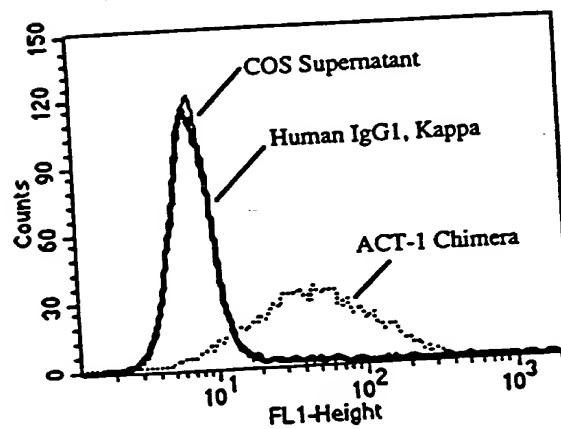


FIGURE 4B

Percent Similarity: 82.143

Percent Identity: 71.429

Act-1.v1

GM607'CL

1 DVVVVTOTPLSLPVSPGDQVSISC[RSSOSLAKSYGNTILS]WYLHKPGOSPO  
 1 DIVMTQSPLSLPVTGPGEPAISIC[RSSQSLLHSNGYNYLD]WYLQKPGOSPO

[ CDR 1 ]

50

50

Act-1.v1

GM607'CL

51 LLIY[GISNRFS]GVPDRFSGSGSGTDFTLKISTIKPEDLGMYIC[LOGTHQP 100  
 51 LLIY[LGSNRAS]GVPDRFSGSGSGTDFTLKISRVEAEDVGVYIC[MQALQTP 100

[ CDR 2 ]

[ CDR 3 ]

Act-1.v1

GM607'CL

101 YT]FGGGTKLEIK 112  
 101 QT]FGQGTKVEIK 112

]

FIGURE 5

Percent Similarity: 82.353

Percent Identity: 68.067

Act-1.vh	1	QVQLQOPGAELVKPGTSLVLSCKGYGTFI[SYAMH]WVKORPCQGLEWIG[E	50
21/28'CL	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFT[SYAMH]WVRQAPGQRLWIG[W	50
		[CDR 1]	
Act-1.vh	51	IDPSESNTNYNOKFKG]KATLTVDISSSTAYMQLSSLTSEDSAVYYCAR[GG	100
21/28'CL	51	INAGNGNTKYSQKFG]RVTITRDTASTAYMELSSLRSEDVAVYYCAR[GG	100
		CDR 2 ]	
Act-1.vh	101	YDGWDYAIDY]WGQGTSTVTVSS	121
21/28'CL	101	Y..YGSGSNY]WGQGTSTVTVSS	119
		CDR 3 ]	

FIGURE 6

1 ATGAAGTTGCCGTGTTAGGCTGTTGGTGCTTCTGTTGTTCTGGATTCTGTTTCCGGAGGT 60  
 TACTTCAACGGACAATCCGACAACCACGAAGACAACAAGACCTAAGGACAAGGCCTCCA  
 [M K L P V R L L V L L L F W I P V S G G]  
 Signal Peptide

61 GATGTTGTGGTGAAGTCAAACCTCCACTCTCCCTGCCCTGTCAGCTTTGGAGATCAAGTTTCT 120  
 CTACAACACCACTGAGTTTGAGGTGAGAGGGACGGACAGTCGAAACCTCTAGTTCAAAGA  
 [D V V V T Q T P L S L P V S F G D Q V S]  
 Framework 1

121 ATCTCTTGCAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCTATTGTCTTGG 180  
 TAGAGAACGTCCAGATCAGTCTCAGAACGTTTCTCAATACCCTTGTGGATAAACAGAACC  
 I S C][R S S Q S L A K S Y G N T Y L S][W  
 CDR 1

181 TACCTGCACAAGCCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCACACAGATT 240  
 ATGGACGTGTTCCGACCGGTGAGAGGTGTCGAGGAGTAGATACCCTAAAGGTTGTCTAAA  
 Y L H K P G Q S P Q L L I Y][G I S N R F  
 CDR 2  
 Framework 2

241 TCTGGGGTGCCAGACAGGTTTCACTGGCAGTGGTTCAGGGACAGATTTCACACTCAAGATC 300  
 AGACCCACGGTCTGTCCAAGTCACCGTCACCAAGTCCCTGTCTAAAGTGTGAGTTCTAG  
 S][G V P D R F S G S G S G T D F T L K I  
 Framework 3

301 AGCACAATAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCCG 360  
 TCGTGTTATTTTCGACTCCTGAACCTTACATAATGACGAATGTTCCATGTGTAGTCGGC  
 S T I K P E D L G M Y Y C][L Q G T H Q P  
 CDR3

361 TACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA 396  
 ATGTGCAAGCCTCCCCCTGGTTCGACCTTTATTTT  
 Y T][F G G G T K L E I K]  
 Framework 4

FIGURE 7

1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGGCCTCC 60  
 CTATAACACTACTGAGTCAGAGGTGAGAGGGACGGGCAGTGGGGACCTCTCGGCCGGAGG  
 (D I V H T Q S P L S L P V T P G E P A S

## Framework 1

61 ATCTCCTGCAGGTCTAGTCAGAGCCTCCTCCATAGTAATGGATCAAACCTATTGGATTGG 120  
 TAGAGGACGTCCAGATCAGTCTCGGAGGAGGTATCATTACCTAGTTTGATAAACCTAACCC  
 I S C)[R S S Q S L L H S N G Y N Y L D][W

## CDR 1

121 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGGGCC 180  
 ATGGACGTCTTCGGTCCCGTCAGAGGTGTCGAGGACTAGATAAACCCCAAGATTAGCCCGG  
 Y L Q K P G Q S P Q L L I Y)[L G S N R A

## Framework 2

## CDR 2

181 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240  
 AGGCCCCAGGGACTGTCCAAGTCACCGTCACCTAGTCCGTGTCTAAATGTGTCTTTTAG  
 S)[G V P D R F S G S G S G T D F T L K I

## Framework 3

241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACCAACTCCT 300  
 TCGTCTCACCTCCGACTCCTACAACCCCAAATAATGACGTACGTTGAGATGGTTGAGGA  
 S R V E A E D V G V Y Y C)[M Q A L Q T P

## CDR 3

301 CAGACGTTCCGGCCAAGGGACCAAGGTGGAATCAAA 336  
 GTCGCAAGCCGGTTCCTGGTTCACCTTTAGTTT  
 Q T)[F G Q G T K V E I K]

## Framework 4

FIGURE 8



1 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTATCAACAGCTACAAGTGTCCACTCCCAG 60  
 TACCCTACCTGACATAGTAGGAGAAGAACCATAGTTGTGCGATGTTACAGGTGAGGGTC  
 M G W S C I I L F L V S T A T S V H S ] [ Q

## Signal Peptide

61 GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCAGTGAAGCTGTCC 120  
 CAGGTTGACGTGCTCGGACCCGACTCGAACACTTCGGACCTGAAGTCACTTCGACAGG  
 V Q L Q Q P G A E L V K P G T S V K L S

## Framework 1

121 TGCAAGGGTTATGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCCT 180  
 ACGTTCCCAATACCGATGTGGAAGTGGTGGATGACCTACGTGACCCACTTCGTCTCCGGA  
 C K G Y G Y T F T ] [ S Y W M H ] [ W V K Q R P

## CDR 1

181 GGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGAGAGTAATACTAACTACAAT 240  
 CCTGTTCCGGAACCTCACCTAGCCTCTCTAACTAGGAAGACTCTCATTATGATTGATGTTA  
 G Q G L E W I G ] [ E I D P S E S N T N Y N

## CDR 2

## Framework 2

241 CAAAAATTCAAGGGCAAGGCCACATTGACTGTAGACATTTCTCCAGCACAGCCTACATG 300  
 GTTTTAAAGTTCCCGTTCGGGTGTAAGTACATCTGTAAAGGAGGTGCTGTCGGATGTAC  
 Q K F K G ] [ K A T L T V D I S S S T A Y M

## Framework 3

301 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTATTGTGCAAGAGGGGGTTAC 360  
 GTCGAGTGTGCGACTGTAGACTCCTGAGACGCCAGATGATAACAGTTCTCCCCCAATG  
 Q L S S L T S E D S A V Y Y C A R ] [ G G Y

361 GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGCACCTCAGTCACCGTCTCCTCA 420  
 CTGCCTACCCTGATACGATAACTGATGACCCAGTTCCGTGAGTCAGTGGCAGAGGAGT  
 D G W D Y A I D Y ] [ W G Q G T S V T V S S ]

## Framework 4

## CDR 3

FIGURE 9

1 ATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTGGCTATTTTAAAAGGTGTCCAGTGTTCAG 60  
 TACCTCAAACCGACTCGACCGAAAAAGAACACCGATAAAATTTCCACAGGTCACAGTC  
 [M E F G L S W L F L V A I L K G V Q C][Q]

## Signal peptide

61 GTGCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120  
 CACGTGGAACACGTGAGACCCGACTCCACTTCTTCGGACCCCGGAGTCACTTCCAAAGG  
 V Q L V Q S G A E V K K P G A S V K V S

## Framework 1

121 TGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGCCCCC 180  
 ACGTTCCGAAGACCTATGTGAAGTGATCGATACGATACGTAACCCACGCGGTCCGGGGG  
 C K A S G Y T F T][S Y A M H][W V R Q A P

## CDR 1

181 GGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAATATTCA 240  
 CCTGTTTCCGAACCTACCTACCCTACCTAGTTGCGACCGTTACCATTGTGTTTATAAGT  
 G Q R L E W M G][W I N A G N G N T K Y S

## Framework 2

## CDR 2

241 CAGAAGTTCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGCCTACATG 300  
 GTCTTCAAGTCCCGTCTCAGTGGTAATGGTCCCTGTGTAGGCGCTCGTGTGGATGTAC  
 Q K F Q G][R V T I T R D T S A S T A Y M

301 GAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAGGAGGTTAC 360  
 CTCGACTCGTCCGACTCTAGACTTCTGTGCCGACACATAATGACACGCTCTCCTCCAATG  
 E L S S L R S E D T A V Y Y C A R][G G Y

## Framework 3

361 TATGGTTCGGGGAGCAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414  
 ATACCAAGCCCCTCGTTGATGACCCCGGTCCCTTGGGACCAAGTGGCAGAGGAGT  
 Y G S G S N Y][W G Q G T L V T V S S]

## CDR 3

## Framework 4

FIGURE 10

Sequence Range: 1 to 540

10 20 30 40  
 ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG GTA TCA ACA GCT ACA AGT  
 M K C T W V I L F L V S T A T S>  
 50 60 70 80 90  
 GTC CAC TCG CAG GTC CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG  
 V H S Q V L V Q S G A E V K K>  
 100 110 120 130 140  
 CCT GGG GCT TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC  
 P G A S V K V S C K G S G Y T F>  
 150 160 170 180 190  
 ACC AGC TAC TGG ATG CAT TGG GTG AGG CAG GCG CCT GGC CAA CGT CTA  
 T S Y W M H W V R Q A P G Q R L>  
 200 210 220 230 240  
 GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT AAC TAC AAT  
 E W I G E I D P S E S N T N Y N>  
 250 260 270 280  
 CAA AAA TTC AAG GGA CGC GTC ACA TTG ACT GTA GAC ATT TCC GCT AGC  
 Q K F K G R V T L T V D I S A S>  
 290 300 310 320 330  
 ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACT GCG GTC  
 T A Y M E L S S L R S E D T A V>  
 340 350 360 370 380  
 TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT GCT ATT GAC  
 Y Y C A R G G Y D G W D Y A I D>  
 390 400 410 420 430  
 TAC TGG GGT CAA GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG  
 Y W G Q G T L V T V S S A S T K>  
 440 450 460 470 480  
 GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG  
 G P S V F P L A P S S K S T S G>  
 490 500 510 520  
 GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG  
 G T A A L G C L V K D Y F P E P>  
 530 540  
 GTG ACG GTG TCG  
 V T V S>

*Signal peptidase cleavage site*  
*Start*  
*AlaI*  
*Const region*  
*BS410*  
*AsaI*

FIGURE 11

Sequence Range: 1 to 413

10 20 30 40  
 \* \* \* \*  
 ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG TTC TGG ATT CCT  
 M K L P V R L L V L L F W I P>  
 50 60 70 80 90  
 \* \* \* \* \*  
 GTT TCC GGA GGT GAT GTT GTG ATG ACT CAA AGT CCA CTC TCC CTG CCT  
 V S G G D V V M T Q S P L S L P>  
 100 110 120 130 140  
 \* \* \* \* \*  
 GTC ACC CCT GGA GAA CCA GCT TCT ATC TCT TGC AGG TCT AGT CAG AGT  
 V T P G E P A S I S C R S S Q S>  
 150 160 170 180 190  
 \* \* \* \* \*  
 CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG TAC CTG CAG AAG  
 L A K S Y G N T Y L S W Y L Q K>  
 200 210 220 230 240  
 \* \* \* \* \*  
 CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC AGA TTT  
 P G Q S P Q L L I Y G I S N R F>  
 250 260 270 280  
 \* \* \* \* \*  
 TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA GGG ACA GAT TTC  
 S G V P D R F S G S G S G T D F>  
 290 300 310 320 330  
 \* \* \* \* \*  
 ACA CTC AAG ATC TCG CGA GTA GAG GCT GAG GAC GTG GGA GTG TAT TAC  
 T L K I S R V E A E D V G V Y Y>  
 340 350 360 370 380  
 \* \* \* \* \*  
 TGC TTA CAA GGT ACA CAT CAG CCG TAC ACG TTC GGA CAG GGG ACC AAG  
 C L Q G T H Q P Y T F G Q G T K>  
 390 400 410  
 \* \* \*  
 GTG GAA ATA AAA CGG GCT GAT GCG GCG CC  
 V E I K R A D A A P>

*Signal peptide cleavage site*  
*Base 1*  
*Asp 718*  
*Met 200*  
*Met*  
*410 kact*

FIGURE 12

## LIGHT CHAIN OLIGOS.

- L1 5'- TTT CCG GAG GTG ATG TTG TGA TGA CTC AAA GTC CAC TCT CCC  
TGC CTG TCA CCC CTG GAG AAC CAG CTT CTA TCT CTT GCA  
GGT CTA GTC AGA G
- L2 5'- ACT GGC CAG GCT TCT GCA GGT ACC AAG ACA AAT AGG TGT TCC  
CAT AAC TCT TTG CAA GAC TCT GAC TAG ACC TGC AAG AGA  
TAG AAG CTG GTT C
- L3 5'- CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC  
AGA TTT TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT  
TC
- L4 5'- ACT CGC GAG ATC TTG AGT GTG AAA TCT GTC CCT GAA CCA CTG  
CCA CTG AAC CTG TCT GGC ACC CCA GAA AAT CTG TTG GAA  
ATC
- L5 5'- TCT CGC GAG TAG AGG CTG AGG ACG TGG GAG TGT ATT ACT GCT  
TAC AAG GTA CAC ATC AGC CGT ACA C
- L6 5'- ATG GCG CCG CAT CAG CCC GTT TTA TTT CCA CCT TGG TCC CCT  
GTC CGA ACG TGT ACG GCT GAT GTG TAC CTT GTA AGC AGT  
AAT AC

LA

LB

LC

## HEAVY CHAIN OLIGOS

DOUBLE STRAND  
FRAGMENT

- H1 5'- ATA AGC TTC GCC ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG  
GTA TCA ACA GCT ACA AGT GTC CAC TCC CAG GTC CAA CTA  
GTG CAC CGG TTA
- H2 5'- TAA CCG GTG CAC TAG TTG GAC CTG GGA GTG GAC ACT TGT AGC  
TGT TGA TAC CAA GAA GAG AAT GAC CCA GGT GCA TTT CAT  
GGC GAA GCT TAT
- H3 5'- CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG CCT GGG GCT  
TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC  
ACC AGC
- H4 5'- TAA CCG GTA CTC TAG ACG TTG GCC AGG CGC CTG CCT CAC CCA  
ATG CAT CCA GTA GCT GGT GAA GGT GTA GCC AGA ACC CTT  
GCA GGA C
- H5 5'- CGT CTA GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT  
ACT AAC TAC AAT CAA AAA TTC AAG GGA CGC GTC A
- H6 5'- TAA CCG GTG TGC TAG CGG AAA TGT CTA CAG TCA ATG TGA CGC  
GTC CCT TGA ATT TTT GAT TGT AGT TAG TAT TAC T
- H7 5'- CCG CTA GCA CAG CCT ACA TGG AGC TCA GCA GCC TGA GAT CTG  
AGG ACA CTG CGG TCT ACT ATT GTG CAA GAG GGG GTT ACG  
ACG GAT G
- H8 5'- TCA CCG GTG CGG TGA CCA GGG TGC CTT GAC CCC AGT AGT CAA  
TAG CAT AGT CCC ATC CGT CGT AAC CCC CTC TTG CAC AAT  
AGT AGA C
- H9 5'- CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC  
TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC  
ACA G
- H10 5'- TCA CCG GTT CGG GGA AGT AGT CCT TGA CCA GGC AGC CCA  
GGG CCG CTG TGC CCC CAG AGG TGC TCT TGG AGG AGG GTG  
CCA GGG G

HA

HB

HC

HD

HE

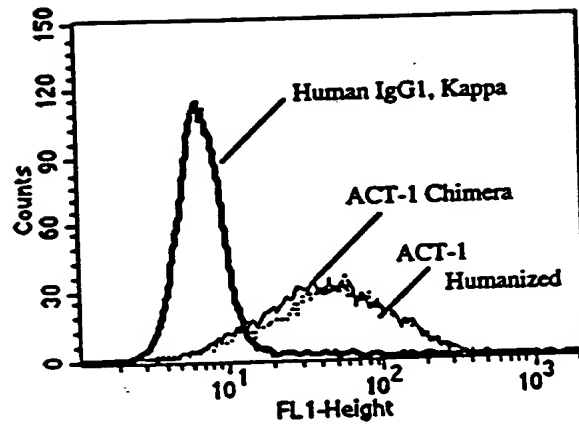


FIGURE 14

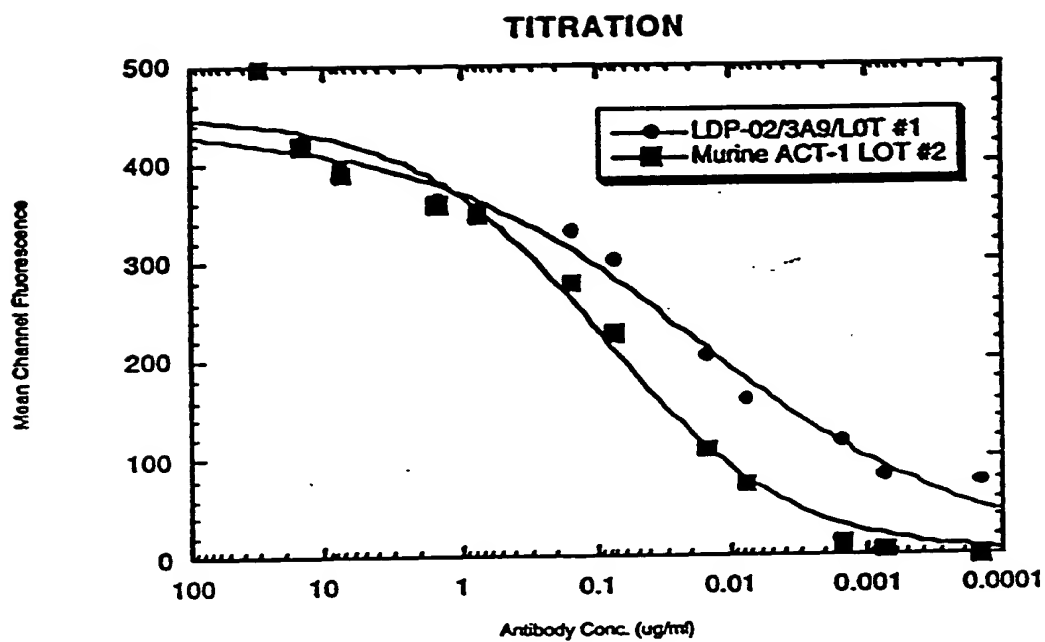


FIGURE 15

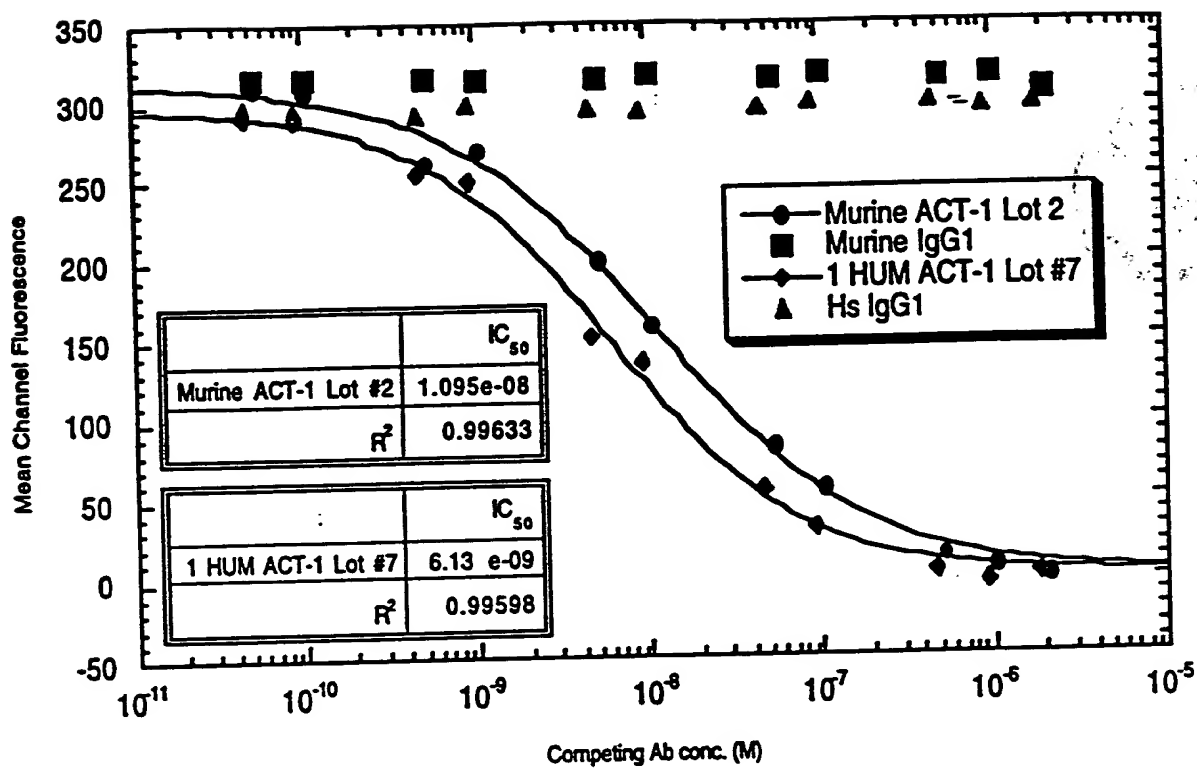


FIGURE 16



# LDP-02 DOES NOT PARTICIPATE IN COMPLEMENT MEDIATED CELL LYSIS

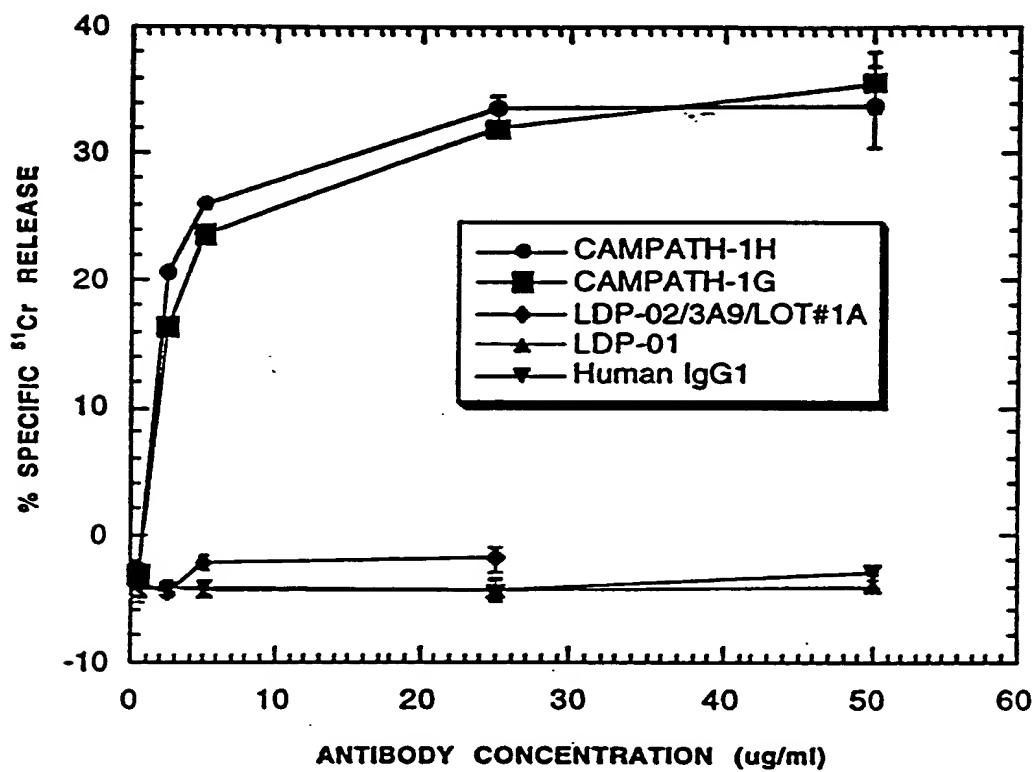


FIGURE 17

—●— Murine ACT-1 Lot #5.1  
—■— Murine IgG1

## ADHESION ASSAY

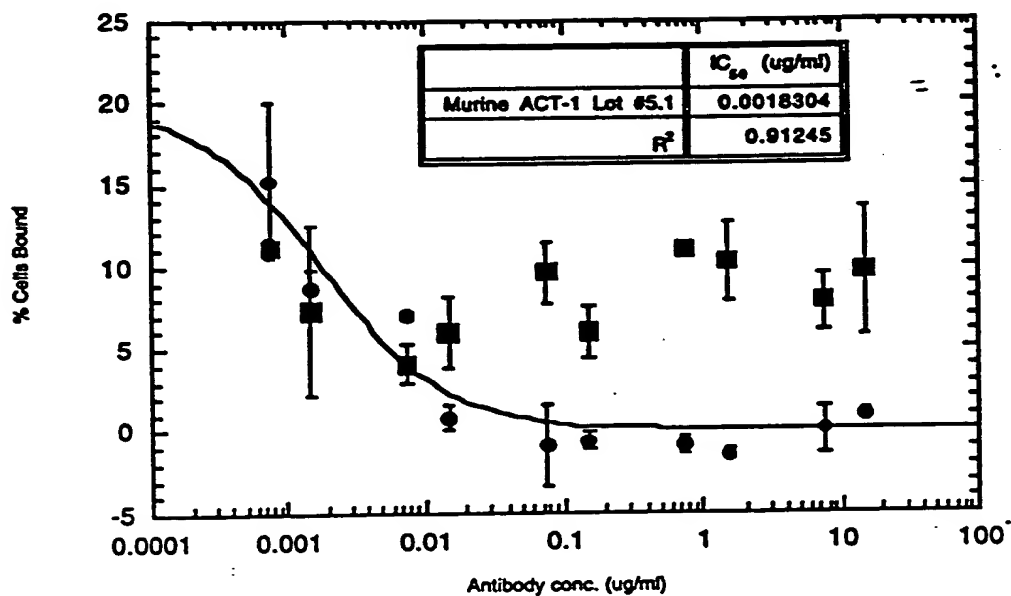


FIGURE 18A

● LDP-02/3A9/Lot#1A  
■ Hs IgG1

## ADHESION ASSAY

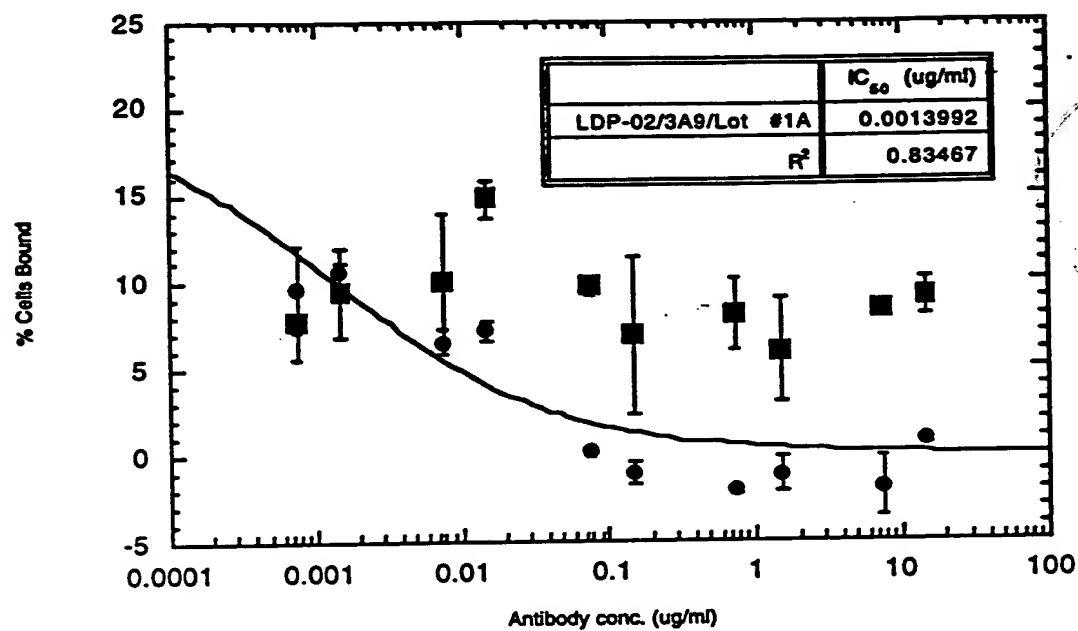


FIGURE 18B

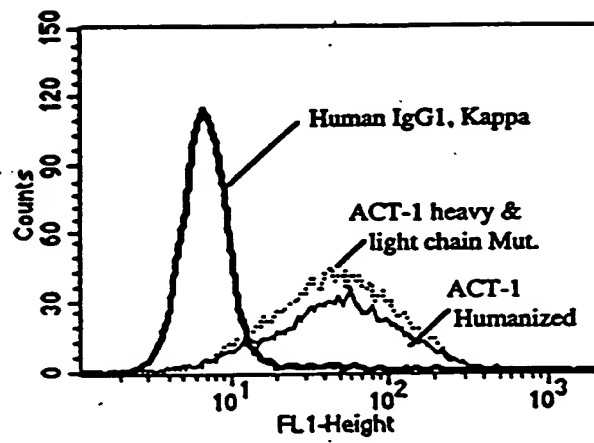


FIGURE 19